

5' TGG CGC TTG CCG AGT GAT TCT CCT CGA ATA CCT CCT GCC GGC GCG GAG ACA CCG  
10 19 28 37 46 55  
GGG CGG GGG TCC TGC CGC AAC TAC CTC CCT TCC TCC TCT CCC CCG CCC CCG GAG  
64 73 82 91 100 109  
CCT TCA TCC TTC CCT TCC CCC CCC ACC TCG AGG GGC GGG CCT GGT TCC CGG GAC  
118 127 136 145 154 163  
ACC ATG TCG GAC TCT GAG GAG GAG AGC CAG GAC CGG CAA CTG AAA ATC GTC GTG  
M S D S E E E S Q D R Q L K I V V  
172 181 190 199 208 217  
CTG GGG GAC GNN GCC TCC GGG AAG ACC TCC TTA ACT ACG TGT TTT GCT CAA GAA  
L G D X A S G K T S L T T C F A Q E  
226 235 244 253 262 271  
ACT TTT GGG AAA CAG TAC AAA CAA ACT ATA GGA CTG GAT TTC TTT TTG AGA AGG  
T F G K Q Y K Q T I G L D F F L R R  
280 289 298 307 316 325  
ATA ACA TTG CCA GGA AAC TTG AAT GTT ACC CTT CAA ATT TGG GAT ATA GGA GGG  
I T L P G N L N V T L Q I W D I G G  
334 343 352 361 370 379  
CAG ACA ATA GGA GGC AAA ATG TTG GAT AAA TAT ATC TAT GGA GCA CAG GGA GTC  
Q T I G G K M L D K Y I Y G A Q G V  
388 397 406 415 424 433  
CTC TTG GTA TAT GAT ATT ACA AAT TAT CAA AGC TTT GAG AAT TTA GAA GAT TGG  
L L V Y D I T N Y Q S F E N L E D W  
442 451 460 469 478 487  
TAT ACT GTG GTG AAG AAA GTG AGC NAG GAG TCA GAA ACT CAG CCA CTG GTT GCC  
Y T V V K K V S X E S E T Q P L V A  
496 505 514 523 532 541  
TTG GTA GGC AAT AAA ATT GAT TTG GAG CAT ATG CGA ACA ATA AAA CCT GAA AAA  
L V G N K I D L E H M R T I K P E K  
550 559 568 577 586 595  
CAC TTA CGG TTT TGC CAG GAA AAT GGT TTT AGT AGC CAC TTT GTC TCA GCC AAG  
H L R F C Q E N G F S S H F V S A K  
604 613 622 631 640 649  
ACA GGA GAC TCT GTC TTC CTG TGC TTT CAG AAA GTT GCT GCT GAA ATC CTT GGG  
T G D S V F L C F Q K V A A E I L G  
658 667 676 685 694 703

FIGURE 1A



5' GCA TTG AGC CAA CAC ACA GAT TTG TCG CCT CTG TCC CCG AAG ACA CCT GCA CCC

10 19 28 37 46 55

TCC ATG CGG ANC AAG ATG GGG AAT GGA ACT GAG GAA GAT TAT AAC TTT GTC TTC

64 73 82 91 100 109

M R X K M G N G T E E D Y N F V F

AAG GTG GTG CTG ATC GGC GAA TCA GGT GTG GGG AAG ACC AAT CTA CTC TCC CGA

118 127 136 145 154 163

K V V L I G E S G V G K T N L L S R

TTC ACG CGC AAT GAG TTC AGC CAC GAC AGC CGC ACC ACC ATC GGG GTT GAG TTC

172 181 190 199 208 217

F T R N E F S H D S R T T I G V E F

TCC ACC CGC ACT GTG ATG TTG GGC ACC GCT GCT GTC AAG GCT CAG ATC TGG GAC

226 235 244 253 262 271

S T R T V M L G T A A V K A Q I W D

ACA GCT GGC CTG GAG CGG TAC CGA GCC ATC ACC TCG GCG TAC TAT CGT GGT GCA

280 289 298 307 316 325

T A G L E R Y R A I T S A Y Y R G A

GTG GGG GCC CTC CTG GTG TTT GAC CTA ACC AAG CAC CAG ACC TAT GCT GTG GTG

334 343 352 361 370 379

V G A L L V F D L T K H Q T Y A V V

GAG CGA TGG CTG AAG GAG CTC TAT GAC CAT GCT GAA GCC ACG ATC GTC GTC ATG

388 397 406 415 424 433

E R W L K E L Y D H A E A T I V V M

CTC GTG GGT AAC AAA AGT GAC CTC GAC CAG GGC CGG GAA GTG CCC ACT GAG GAG

442 451 460 469 478 487

L V G N K S D L S Q G R E V P T E E

GCC CGA ATG TTC GCT GAA AAC AAT GGA CTG CTC TTC CTG GAG ACC TCA GCC CTG

496 505 514 523 532 541

A R M F A E N N G L L F L E T S A L

GAC TCT ACC AAT GTT GAG CTA GCC TTT GAG ACT GTC CTG AAA GAA ATC TTT GCG

550 559 568 577 586 595

D S T N V E L A F E T V L K E I F A

AAG GTG TCC AAG CAG AGA CAG AAC AGC ATC CGG ACC AAT GCC ATC ACT CTG GGC

604 613 622 631 640 649

K V S K Q R Q N S I R T N A I T L G

AGT GCC CAG GNT GGA CAG GAG CCT GGC CCT GGG GAG AAG AGG GCC TGT TGC ATC

658 667 676 685 694 703

S A Q X G Q E P G P G E K R A C C I

FIGURE 2A

FIGURE 2A

Docket No.: PF-0183-2 DIV  
Inventors: Hillman et al.  
Title: RAB PROTEINS  
Serial No.: To Be Assigned

712 721 730 739 748 757  
AGC CTC TGA CCT TGG CCA GCA CCA CCT GCC CCC ACT GGC TTT TTG GTG CCC CTT  
S L

766 775 784 793 802 811  
GTC CCC ACT TCA GCC CCA GGA CCT TTC CTT GCC CTT TGG TTC CAG ATA TCA GAC

820 829 838 847  
TGT TCC CTG TTC ACA GCA CCC TCA GGG TCT TAA GGT 3'

FIGURE 2B

5' CTG TGA TGA AAC ACT TTT CCC GTG TCG TTT GAG TGC ATC TTC TCA ACA ACC CTA

GGA GGG TTC TTG AAG CTT TTG AGA TTA ACA ATG GCA GGA AAA TCA TCA CTT TTT

AAA GTA ATT CTC CTT GGA GAT GGT GGA GTT GGG AAG AGT TCA CTT ATG AAC AGA

K V I L L G D G G V G K S S L M N R

TAT GTA ACT AAT AAG TTT GAT ACC CAG CTC TTC CAT ACA ATA GGT GTG GAA TTT

Y V T N K F D T Q L F H T I G V E F

TTA AAT AAA GAT TTG GAA GTG GAT GGA CAT TTT GTT ACC ATG CAG ATT TGG GAC

L N K D L E V D G H F V T M Q I W D

ACG GCA GGT CAG GAG CGA TTC CGA AGC CTG AGG ACA CCA TTT TAC AGA GGT TCT

T A G Q E R F R S L R T P F Y R G S

GAC TGC TGC CTG CTT ACT TTT AGT GTC GAT GAT TCA CAA AGC TTC CAG AAC TTA

D C C L L T F S V D D S Q S F Q N L

AGT AAC TGG AAG AAA GAA TTC ATA TAT TAT GCA GAT GTG AAA GAG CCT GAG AGC

S N W K K E F I Y Y A D V K E P E S

TTT CCT TTT GTG ATT CTG GGT AAC AAG ATT GAC ATA AGC GAA CGG CAG GTG TCT

F P F V I L G N K I D I S E R Q V S

ACA GAA GAA GCC CAA GCT TGG TGC AGG GAC AAC GGC GAC TAT CCT TAT TTT GAA

T E E A Q A W C R D N G D Y P Y F E

ACA AGT GCA AAA GAT GCC ACA AAT GTG GCA GCA GCC TTT GAG GAA GCG GTT CGA

T S A K D A T N V A A A F E E A V R

AGA GTT CTT GCT ACC GAG GAT AGG TCA GAT CAT TTG ATT CAG ACA GAC ACA GTC

R V L A T E D R S D H L I Q T D T V

FIGURE 3A

AAT	CTT	CAC	CGA	AAG	CCC	AAG	CCT	AGC	TCA	TCT	TGC	TGT	TGA	TTG	TTA	GAT	TGT
N	L	H	R	K	P	K	P	S	S	S	C	C					
		713			722			731			740			749			758
TGA	TGC	ATT	CTA	ACC	AAC	TCA	CAC	ATA	TAC	ACA	AAA	TCA	ACA	TGG	GGA	TGG	AGA
		767			776			785			794			803			812
AGA	GAA	TTA	GCG	TTT	GCA	GCA	GTG	TAT	CAT	CTA	CTA	ATA	AAA	TTA	AAC	TAA	TGT
		821			830			839			848			857			866
TGC	TGC	TTC	ATT	AGT	TGG	TGG	GAG	AAG	GGA	CAC	ATC	CAC	TCT	TGG	AGG	AAT	ATA
		875			884			893			902			911			920
TTT	ACT	CAA	TAA	TGG	CAC	CTT	ACA	TTT	ATA	AAT	TGT	AAC	AGT	TGT	CTA	ATA	ACG
		929			938			947			956			965			974
TTT	CTT	TAA	TTT	AAA	TAT	GTA	AGT	TGC	AGA	GCT	AAT	AAA	TGA	AAT	GAC	CAA	GAC
		983			992			1001			1010			1019			1028
TTT	AAT	TAT	AAT	AAA	AAT	AAG	AAA	CTT	GAC	TAT	TCT	AGA	AGT	TAT	ACT	TGG	ATT
		1037			1046			1055			1064			1073			1082
TTT	TCC	TGG	GAA	AAT	GGA	GAA	CTA	CTT	TTT	ATA	TGT	GTA	TGT	TTT	TAT	GCA	ATT
		1091			1100			1109			1118			1127			1136
AGC	ATT	GTA	TTC	TTG	GTT	CAG	GGA	AAT	ACT	TTC	CTA	AAG	CAA	TAA	TGT	TAG	ATA
		1145			1154			1163			1172						
TTA	AAG	ATT	AAA	ATC	TAA	TGT	AAA	AAA	AAA	AAA	AAA	AAA	AAA	3'			

FIGURE 3B

1	M	S	D	S	E	E	S	Q	D	R	Q	-	-	-	L	K	I	V	V	L	G	D	X	A	S	G	K	T	SEQ ID NO-1		
1	M	S	D	S	E	E	S	Q	D	R	Q	-	-	-	L	K	I	V	V	L	G	D	G	T	S	G	K	T	GI 1154901		
1	M	R	X	K	M	G	N	G	T	E	E	D	Y	N	F	V	F	K	V	V	L	I	G	E	S	G	V	G	K	T	SEQ ID NO-3
1	M	G	N	-	-	-	G	K	E	E	D	Y	N	F	V	F	K	V	V	L	I	G	E	S	G	V	G	K	T	GI 436001	
1	M	A	G	K	S	S	-	-	-	-	-	-	-	-	L	F	K	V	I	L	L	G	D	G	G	V	G	K	S	SEQ ID NO-5	
1	M	A	G	K	S	S	-	-	-	-	-	-	-	-	L	F	K	V	I	L	L	G	D	G	G	V	G	K	S	GI 486830	
27	S	L	T	T	C	F	A	Q	E	T	F	G	K	Q	Y	K	Q	T	I	G	L	D	F	F	L	R	R	I	T	L	SEQ ID NO-1
27	S	L	A	T	C	F	A	Q	E	T	F	G	K	Q	Y	K	Q	T	I	G	L	D	F	F	L	R	R	I	T	L	GI 1154901
31	N	L	L	S	R	F	T	R	N	E	F	S	H	D	S	R	T	T	I	G	V	E	F	S	T	R	T	V	M	L	SEQ ID NO-3
27	N	L	L	S	R	F	T	R	N	E	F	S	H	D	S	R	T	T	I	G	V	E	F	S	T	R	T	V	L	L	GI 436001
22	S	L	M	N	R	Y	V	T	N	K	F	D	T	Q	L	F	H	T	I	G	V	E	F	L	N	K	D	L	E	V	SEQ ID NO-5
22	S	L	M	N	R	Y	V	T	N	K	F	D	T	Q	L	F	H	T	I	G	V	E	F	L	N	K	D	L	E	V	GI 486830
57	P	G	N	L	N	V	T	L	Q	I	W	D	I	G	G	Q	T	I	G	G	K	M	L	D	K	Y	I	Y	G	A	SEQ ID NO-1
57	P	G	N	L	N	V	T	L	Q	I	W	D	I	G	G	Q	T	I	G	G	K	M	L	D	K	Y	I	Y	G	A	GI 1154901
61	G	T	A	A	-	V	K	A	Q	I	W	D	T	A	G	L	E	R	Y	R	A	I	T	S	A	Y	Y	R	G	A	SEQ ID NO-3
57	G	T	A	A	-	V	K	A	Q	I	W	D	T	A	G	L	E	R	Y	R	A	I	T	S	A	Y	Y	R	G	A	GI 436001
52	D	G	H	F	-	V	T	M	Q	I	W	D	T	A	G	Q	E	R	F	R	S	L	R	T	P	F	Y	R	G	S	SEQ ID NO-5
52	D	G	H	F	-	V	T	M	Q	I	W	D	T	A	G	Q	E	R	F	R	S	L	R	T	P	F	Y	R	G	S	GI 486830
87	Q	G	V	L	L	V	Y	D	I	T	N	Y	Q	S	F	E	N	L	E	D	W	Y	T	V	V	K	K	V	S	X	SEQ ID NO-1
87	Q	G	I	L	L	V	Y	D	I	T	N	Y	Q	S	F	E	N	L	E	D	W	Y	S	V	V	K	T	V	S	E	GI 1154901
90	V	G	A	L	L	V	F	D	L	T	K	H	Q	T	Y	A	V	V	E	R	W	L	K	E	L	-	-	Y	D	H	SEQ ID NO-3
86	V	G	A	L	L	V	F	D	L	T	K	H	Q	T	Y	A	V	V	E	R	W	L	K	E	L	-	-	Y	D	H	GI 436001
81	D	C	C	L	L	T	F	S	V	D	D	S	Q	S	F	Q	N	L	S	N	W	K	K	E	F	I	Y	Y	A	D	SEQ ID NO-5
81	D	C	C	L	L	T	F	S	V	D	D	S	Q	S	F	Q	N	L	S	N	W	K	K	E	F	I	Y	Y	A	D	GI 486830
117	E	S	E	T	Q	P	L	V	-	A	L	V	G	N	K	I	D	L	E	H	M	R	T	I	K	P	E	K	H	L	SEQ ID NO-1
117	E	S	E	T	Q	P	L	V	-	A	L	V	G	N	K	I	D	L	E	H	M	R	T	V	K	P	D	K	H	L	GI 1154901
118	A	E	A	-	-	T	I	V	V	M	L	V	G	N	K	S	D	L	S	Q	G	R	E	V	P	T	E	E	A	R	SEQ ID NO-3
114	A	E	A	-	-	T	I	V	V	M	L	V	G	N	K	S	D	L	S	Q	A	R	E	V	P	T	E	E	A	R	GI 436001
111	V	K	E	P	E	S	F	P	F	V	I	L	G	N	K	I	D	I	S	E	-	R	Q	V	S	T	E	E	A	Q	SEQ ID NO-5
111	V	K	E	P	E	S	F	P	F	V	I	L	G	N	K	I	D	I	S	E	-	R	Q	V	S	T	E	E	A	Q	GI 486830
146	R	F	C	Q	E	N	G	F	S	S	H	F	-	V	S	A	K	T	G	D	S	V	F	L	C	F	Q	K	V	A	SEQ ID NO-1
146	R	F	C	Q	E	N	G	F	S	S	H	F	-	V	S	A	K	T	G	D	S	V	F	L	C	F	Q	K	V	A	GI 1154901
146	M	F	A	E	N	N	G	-	L	L	F	L	E	T	S	A	L	D	S	T	N	V	E	L	A	F	E	T	V	L	SEQ ID NO-3
142	M	F	A	E	N	N	G	-	L	L	F	L	E	T	S	A	L	D	S	T	N	V	E	L	A	F	E	T	V	L	GI 436001
140	A	W	C	R	D	N	G	D	Y	P	Y	F	E	T	S	A	K	D	A	T	N	V	A	A	A	F	E	E	A	V	SEQ ID NO-5
140	A	W	C	R	D	N	G	D	Y	P	Y	F	E	T	S	A	K	D	A	T	N	V	A	A	A	F	E	E	A	V	GI 486830
175	A	E	I	L	G	I	K	L	N	X	X	Q	X	X	X	S	H	X	G	V	V	K	X	X	I	V	N	Y	N	Q	SEQ ID NO-1
175	A	E	I	L	G	I	K	L	N	K	A	E	I	E	Q	S	Q	R	-	V	V	K	A	D	I	V	N	Y	N	Q	GI 1154901
175	K	E	I	F	-	-	-	-	-	-	A	K	V	S	K	Q	R	Q	N	S	I	R	T	N	A	I	T	L	G	S	SEQ ID NO-3
171	K	E	I	F	-	-	-	-	-	-	A	K	V	S	K	Q	I	Q	N	S	P	R	S	N	A	I	A	L	G	S	GI 436001
170	R	R	V	L	-	-	-	-	-	-	A	T	-	E	D	R	S	D	H	L	I	Q	T	D	T	V	N	L	-	-	SEQ ID NO-5
170	R	R	V	L	-	-	-	-	-	-	A	T	-	E	D	R	S	D	H	L	I	Q	T	D	T	V	S	L	-	-	GI 486830
205	E	P	M	S	R	T	X	N	P	P	R	S	S	M	C	A	V	Q												SEQ ID NO-1	
204	E	P	M	S	R	T	V	N	P	P	R	S	S	M	C	A	V	Q												GI 1154901	
199	A	Q	X	G	Q	E	P	G	P	G	E	K	R	A	C	C	I	S	L											SEQ ID NO-3	
195	A	Q	A	G	Q	E	P	G	P	G	Q	K	R	A	C	C	I	N	L											GI 436001	
191	-	-	-	-	-	H	R	K	P	K	P	S	S	S	C	C														SEQ ID NO-5	
191	-	-	-	-	-	H	R	K	P	K	P	S	S	S	C	C														GI 486830	

FIGURE 4

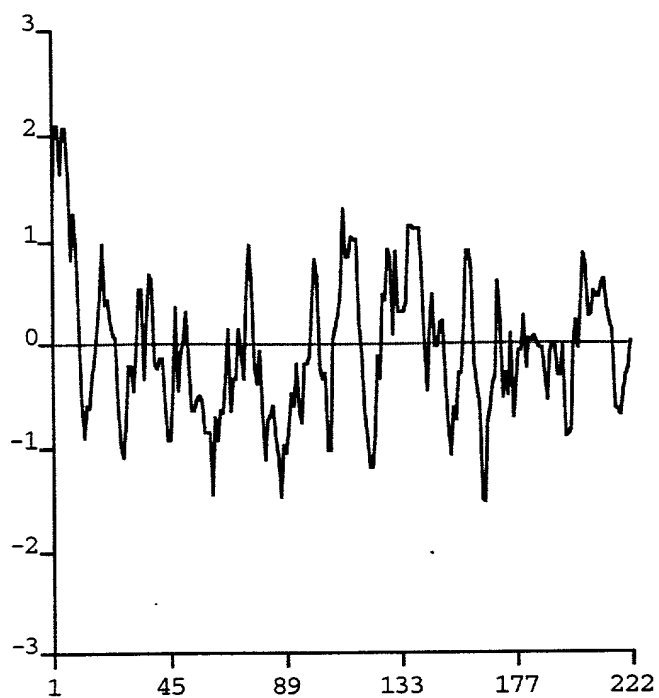


FIGURE 5



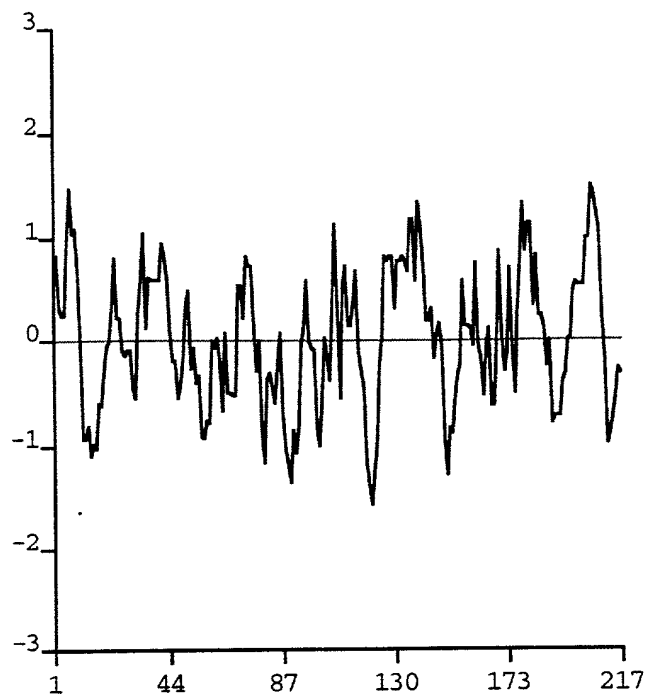


FIGURE 6

TOPP 468660

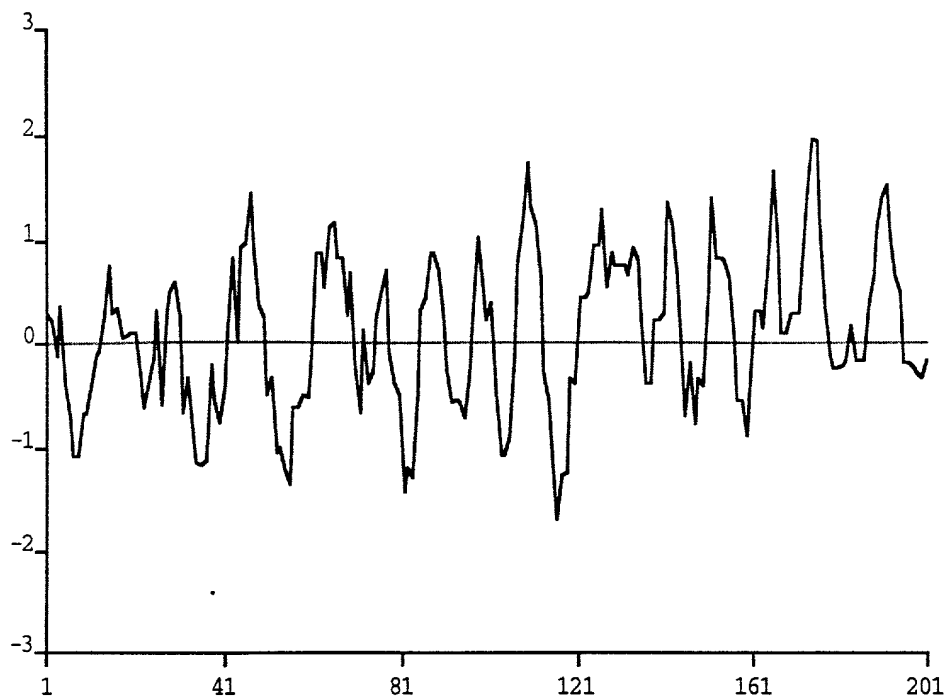


FIGURE 7

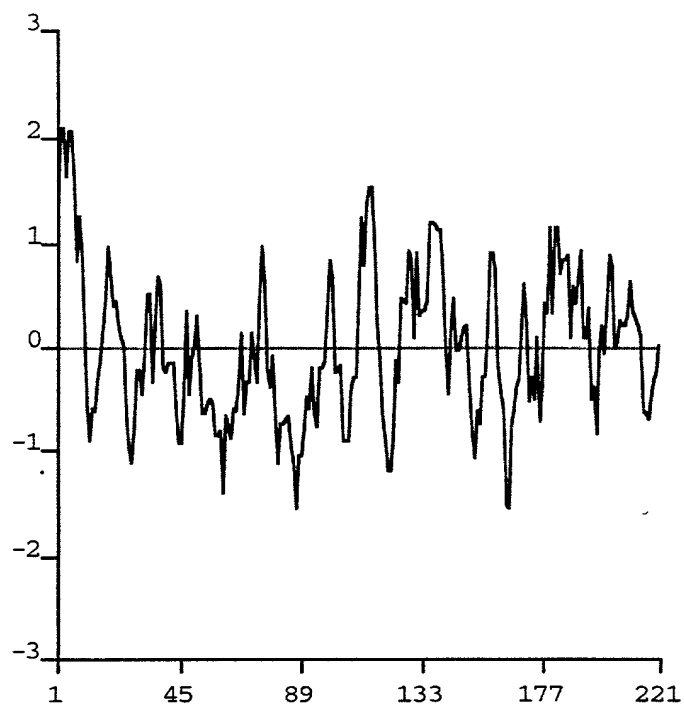


FIGURE 8